

FILE 'HOME' ENTERED AT 13:16:16 ON 14 AUG 2003

=> file medline biosis capplus
COST IN U.S. DOLLARS

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 13:16:33 ON 14 AUG 2003

FILE 'BIOSIS' ENTERED AT 13:16:33 ON 14 AUG 2003
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FILE 'CAPLUS' ENTERED AT 13:16:33 ON 14 AUG 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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=> g protein-coupled receptor
L1 25886 G PROTEIN-COUPLED RECEPTOR

=> polynucleotide
L2 33502 POLYNUCLEOTIDE

=> nucleic acid
L3 351190 NUCLEIC ACID

=> 12 or 13
L4 374190 L2 OR L3

⇒ 11 and 14

=> 15 and 1970-2000/py
2 FILES SEARCHED...

457 HS AND 1970-2000/PY

-> dup rem 16
PROCESSING COMPLETED FOR L6
L7 431 DUP REM L6 (26 DUPLICATES REMOVED)

=> peter?/au and lind?/au
L8 1192 PETER?/AU AND LIND?/AU

=> linda?/au and wood?/au
L9 93 LINDA?/AU AND WOOD?/AU

=> luis?/au and parodi?/au

2 LUIS?/AU AND PARODI?/AU
--> gabriela?/au and marcela?/au

LII 0 GABRIEL?/AU AND VOGELI?/AU

L12 1287 L8 OR L9 OR L10

L13 0 L7 AND L12

→ a mis

(FILED HOME ENTERED AT 13:16:16 ON 14 AUG 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:16:33 ON 14 AUG 2003

L1 25886 G PROTEIN-COUPLED RECEPTOR
L2 33502 POLYNUCLEOTIDE
L3 351190 NUCLEIC ACID
L4 374190 L2 OR L3
L5 1103 L1 AND L4
L6 457 L5 AND 1970-2000/PY
L7 431 DUP REM L6 (26 DUPLICATES REMOVED)
L8 1192 PETER?/AU AND LIND?/AU
L9 93 LINDA?/AU AND WOOD?/AU
L10 2 LUIS?/AU AND PARODI?/AU
L11 0 GABRIEL?/AU AND VOGELI?/AU
L12 1287 L8 OR L9 OR L10
L13 0 L7 AND L12

=> logoff

US-09-884-430-3

Sequence Comparison A

; Sequence 3, Application US/09884430
; Patent No. US20020151046A1
; GENERAL INFORMATION:
; APPLICANT: Glucksman, Maria Alexandra
; APPLICANT: Santiago, Immaculada Silos
; TITLE OF INVENTION: 52871, A NOVEL HUMAN G PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR AND USES THEREOF
; FILE REFERENCE: MNI-165
; CURRENT APPLICATION NUMBER: US/09/884,430
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: USSN 60/212,331
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: USSN 60/269,758
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1044)
US-09-884-430-3

Alignment Scores:

Pred. No.:	1.04e-195	Length:	1044
Score:	1757.00	Matches:	337
Percent Similarity:	98.83%	Conservative:	1
Best Local Similarity:	98.54%	Mismatches:	4
Query Match:	90.80%	Indels:	0
DB:	10	Gaps:	0

US-09-750-373-25 (1-371) x US-09-884-430-3 (1-1044)

Qy	1 MetProAlaAsnPheThrGluGlySerPheAspSerSerGlyThrGlyGlnThrLeuAsp	20
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Qy	21 SerSerProValAlaCysThrGluThrValThrPheThrGluValValGluGlyLysGlu	40
Db	61 TCTTCCCCAGTGGCTTGCACGTGAAAGCAGTGACTTTACTGAAGTGGTAAAGGAAAGGAA	120
Qy	41 TrpGlySerPheTyrTyrSerPheLysThrGluGlnLeuIleThrLeuTrpValLeuPhe	60
Db	121 TGGGGTTCTTCTACTACTCCTTAAGACTGAGCAATTGATAACTCTGTGGTCCTCTTT	180
Qy	61 ValPheThrIleValGlyAsnSerValValLeuPheSerThrTrpArgArgLysLysLys	80
Db	181 GTTTTTACCATTGTTGGAAACTCCGTTGTGCTTTTCCACATGGAGGAGAAAGAAGAAG	240
Qy	81 SerArgMetThrPhePheValThrGlnLeuAlaIleThrAspSerPheThrGlyLeuVal	100
Db	241 TCAAGAATGACCTTCTTGTGACTCAGCTGGCCATCACAGATTTCACAGGACTGGTC	300

Qy 101 AsnIleLeuThrAspIleIleTrpArgPheThrGlyAspPheThrAlaProAspLeuVal 120
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 Db 301 AACATCTTGACAGATATTATTTGGCGATTCACCGGAGACTCACGGCACCTGACCTGGTT 360

 Qy 121 CysArgValValArgTyrLeuGlnValValLeuLeuTyrAlaSerThrTyrValLeuVal 140
 |||||
 Db 361 TGCCGAGTGGTCCGCTATTGCAGGTTGTGCTGCTGTACGCCTCACCTACGTCCTGGTG 420

 Qy 141 SerLeuSerIleAspArgTyrHisAlaIleValTyrProMetLysPheLeuGlnGlyGlu 160
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 Db 421 TCCCTCAGCATAGACAGATACCATGCCATCGTCTACCCATGAAGTTCCCTCAAGGAGAA 480

 Qy 161 LysGlnAlaArgValLeuIleValIleAlaTrpSerLeuSerPheLeuPheSerIlePro 180
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 Db 481 AAGCAAGCCAGGGTCCTCATTGTGATGCCCTGGAGCCTGTCTTCTGTTCTCCATTCCC 540

 Qy 181 ThrLeuIleIlePheGlyLysArgThrLeuSerAsnGlyGluValGlnCysTrpAlaLeu 200
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 Db 541 ACCCTGATCATATTGGGAAGAGGGACACTGTCCAACGGTGAAGTGCAGTGCTGGCCCTG 600

 Qy 201 TrpProGlyAspSerTyrTrpThrProTyrMetThrIleValAlaPheLeuValTyrPhe 220
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 Db 601 TGGCCTGACGACTCCTACTGGACCCATACATGACCATCGTGGCCTCCTGGTGTACTTC 660

 Qy 221 IleProLeuThrIleIleSerIleMetTyrGlyIleValIleArgThrIleTrpIleLys 240
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 Db 661 ATCCCTCTGACAATCATCAGCATCATGTATGGCATTGTGATCCGAACTATTGGATTAAA 720

 Qy 241 SerLysThrTyrGluThrValIleSerAsnCysSerAspGlyLysLeuCysSerSerTyr 260
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 Db 721 AGGAAAACCTACGAAACAGTGATTCCAAGTGCAGATGGAAACTGTGCAGCAGCTAT 780

 Qy 261 AsnArgGlyLeuIleSerLysAlaLysIleLysAlaIleLysTyrSerIleIleIle 280
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 Db 781 AACCGAGGACTCATCTCAAAGCAAAATCAAGGCTATCAAGTATAGCATCATCATCATT 840

 Qy 281 LeuAlaPheIleCysCysTrpSerProTyrPheLeuPheAspIleLeuAspAsnPheAsn 300
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 Db 841 CTTGCCCTCATCTGCTGGAGTCATACTCCCTGTTGACATTGGACAATTCAAC 900

 Qy 301 LeuLeuProAspThrGlnGluArgPheTyrAlaSerValIleIleGlnAsnLeuProAla 320
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 Db 901 CTCCTTCCAGACACCCAGGAGCGTTCTATGCCCTGTGATCATTAGAACCTGCCAGCA 960

 Qy 321 LeuAsnSerAlaIleAsnProProIleTyrCysValPheSerSerSerIleSerPhePro 340
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 Db 961 TTGAATAGTGCCATCAACCCCTCATCTACTGTGCTTCAGCAGCTCCATCTCTTCCCC 1020

 Qy 341 CysArg 342
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 Db 1021 TGCAGG 1026

Sequence Comparison B

LOCUS AI500347 **414 bp** **mRNA** **linear** **EST 14-APR-1999**
DEFINITION tm95f03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165885
3',
mRNA sequence.
ACCESSION AI500347
VERSION AI500347.1 GI:4392329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information can
be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1403 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 399.
FEATURES
source Location/Qualifiers
1. .414
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2165885"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendrogloma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac
(Pharmacia) with a
RI; 1st
primer [5'
modified polylinker; Site_1: Not I; Site_2: Eco
strand cDNA was primed with a Not I - oligo(dT)
TGTACCAATCTGAAGTGGAGCGGCCGCATAGTTTTTTTTTTTTTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and
cloned into
vector.
Bento
the Not I and Eco RI sites of the modified pT7T3
Library is normalized, and was constructed by

Soares and M.Fatima Bonaldo."

BASE COUNT 86 a 96 c 129 g 103 t
ORIGIN

Query Match 23.5%; Score 391.8; DB 9; Length 414;
Best Local Similarity 98.1%; Pred. No. 2.3e-76;
Matches 407; Conservative 0; Mismatches 7; Indels 1;
Gaps 1;

Qy 1206 CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTAGACCCTAGGGCAGTGCCAGTGC 1265
|||
Db 414 CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTTGCACCTAGGGCAGTGCCAGTGC 355
|||
Qy 1266 TAGGCTGAGCACCACATCAGCTCTCCCAGGTCTTGTCAACCTGCTTGGGCACGTGCATGGAA 1325
|||
Db 354 TAGGCTGAGCACCACATCAGCTCTCCCAGGTCTTGTCAACCTGCTTGGGCACGTGCATGGAA 295
|||
Qy 1326 CCCGAGCCAACTTCACCCCCACCCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT 1385
|||
Db 294 CCCGAGCCAACTCACCCCCCACCCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT 235
|||
Qy 1386 AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACCTCCCCAGTTATTGCAG 1445
|||
Db 234 AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACCTCCCCAGTTATTGCAG 175
|||
Qy 1446 CCAGGAAGGAAACGCCCTCCTTCCCCACCATTCCAGGCCCTCCCTCCACTGGCCAGCAC 1505
|||
Db 174 CCAGGAAGGAAACGCC-TCCTTCCCCACCATTCCAGGCCCTCCCTCCACTGGCCAGCAC 116
|||
Qy 1506 CTGAACCCAGTGAACACAGGCATTAGTGGTCCAGGGCCTGGCTTGGAGCCAGTGAGTAG 1565
|||
Db 115 CTGAACCCAGTGAACACAGGCATCAGTGGTCCAGGGCCTGGCTTGGAGCCAGTGAGTAG 56
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Qy 1566 ACAGGCAAGCAGAGGGGACAAAGGTAGCTGGTTATACATGAATATTCTCATTAC 1620
|||
Db 55 ACAGGCAAGCAGAGGGGACAAAGGTAGCTGGTTATACATGAATATTCTCATTAC 1

WEST Search History

DATE: Thursday, August 14, 2003

<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
side by side		result set	
<i>DB=USPT; PLUR=YES; OP=AND</i>			
L12	l6 and L11	0	L12
L11	17 or 18 or 19	42	L11
L10	gabriel.in. and vogeli.in.	0	L10
L9	luis.in. and parodi.in.	3	L9
L8	linda.in. and wood.in.	17	L8
L7	peter.in. and lind.in.	22	L7
L6	L5 and isolated	1038	L6
L5	l1 and L4	1098	L5
L4	l2 or L3	48153	L4
L3	nucleic adj acid	46574	L3
L2	polynucleotide	17758	L2
L1	g adj protein adj coupled adj receptor	1594	L1

END OF SEARCH HISTORY